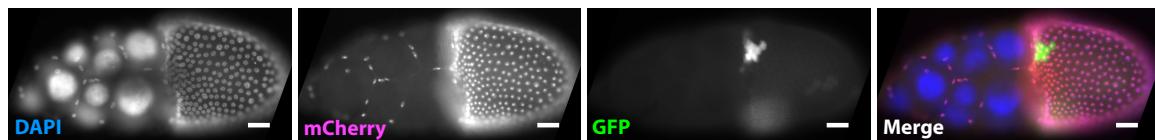
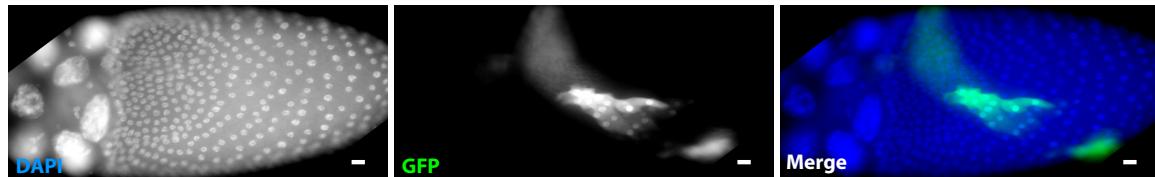


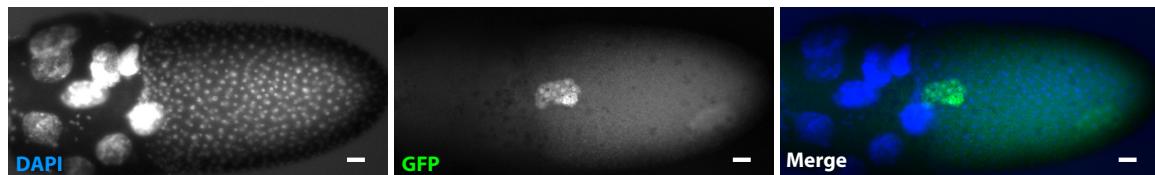
A *tj-GAL4,dcr2^{-/-}; UAS-mCherry::NLS; UAS-FHVΔB2eGFP*



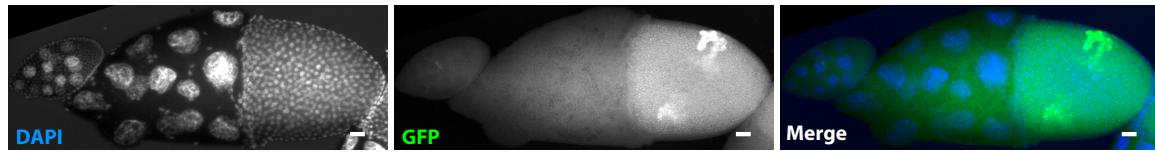
B *tj-GAL4;UAS-FHVΔB2eGFP; Ago2^{-/-}*



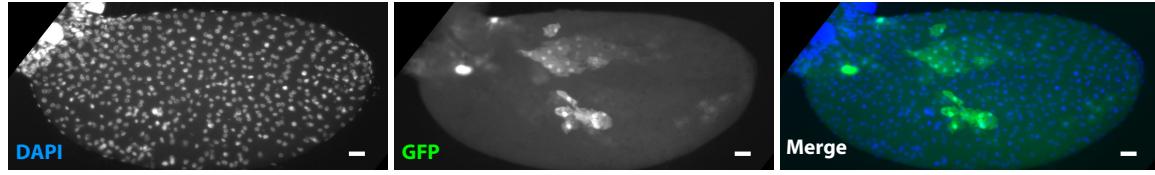
C *tj-GAL4/Su(Var)205; UAS-FHVΔB2eGFP,UAS-CrPV-1A*



tj-GAL4/CyO; UAS-FHVΔB2eGFP,UAS-CrPV-1A



tj-GAL4; UAS-FHVΔB2eGFP,UAS-CrPV-1A/Su(Var)3-9



tj-GAL4; UAS-FHVΔB2eGFP,UAS-CrPV-1A/TM3

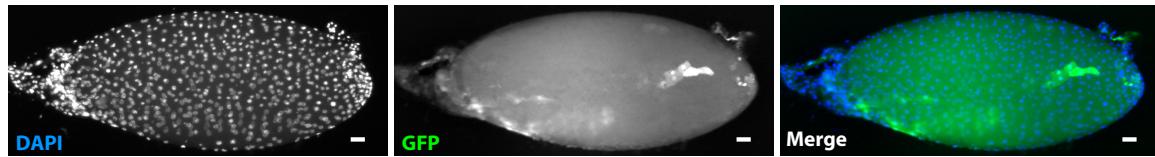


Figure S1 - Variegated expression of the FHVΔB2eGFP replicon in follicular somatic cells of the ovary, in siRNA deficient flies, is not due to position effects of the transgenes. *tj-GAL4* driven expression of FHVΔB2eGFP in follicular somatic cells during oogenesis. Green fluorescence patches are observed when the replicon is co-expressed with UAS-mCherry::NLS in *dcr2* null mutants (A), in lines with insertions of FHVΔB2eGFP in the 2nd chromosome in a *Ago2* null mutant background (B) and when co-expressed with UAS-CrPV-1A in two dominant suppressor of variegation backgrounds (*Su(Var)205* and *Su(Var)3-9*) or in their genetic background controls (CyO or TM3)(C). Scale bar=25μm

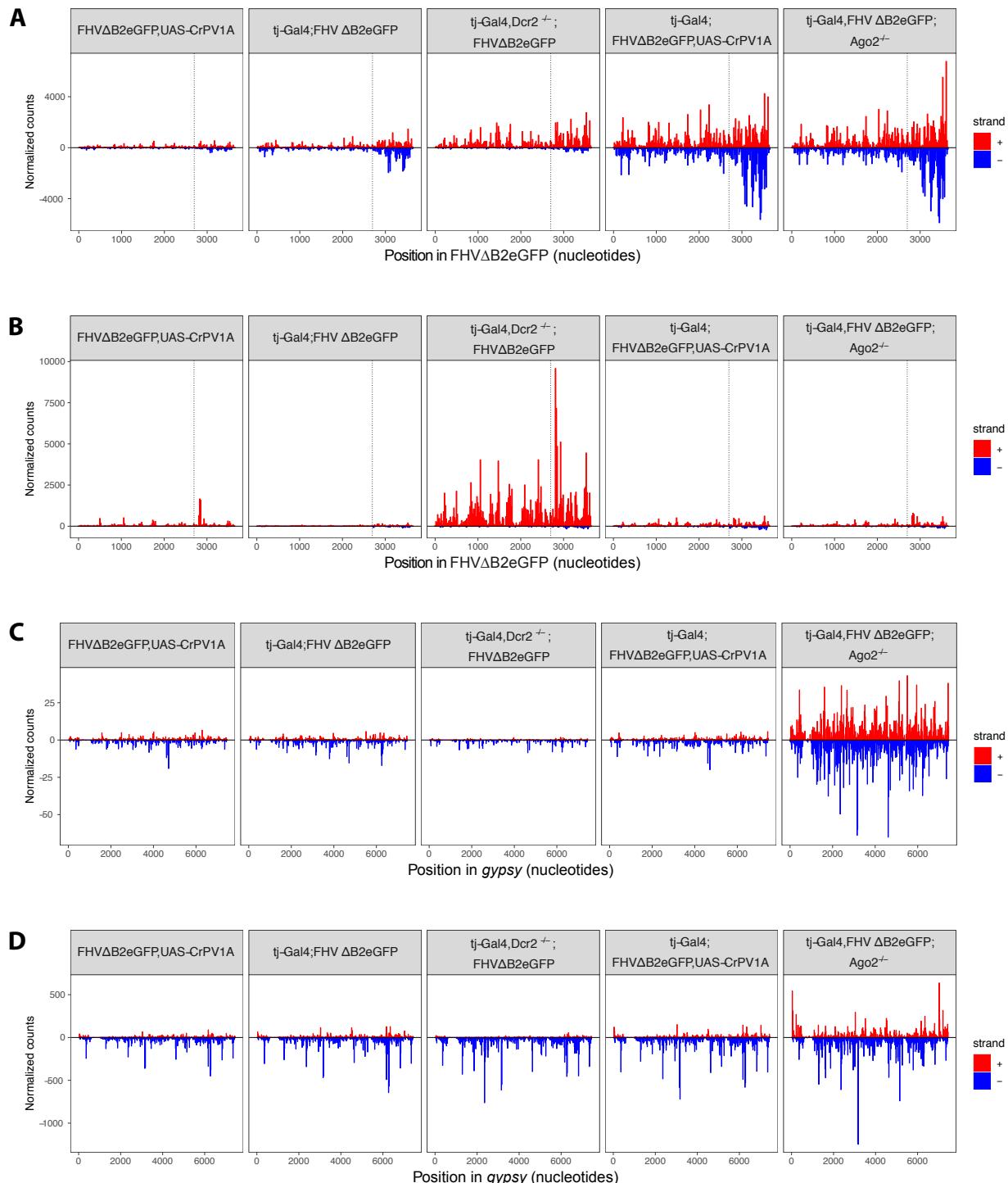


Figure S2 - small RNA coverage of FHV Δ B2eGFP and gypsy. Mean normalized coverage of the FHV Δ B2eGFP replicon and gypsy transposable element by 21 nucleotides (siRNA-like, **A** and **C**, respectively) and 24-28 nucleotide (piRNA-like, **B** and **D**) reads, across 20bp windows. Dotted lines in panels **A** and **B** mark the first nucleotide of B2(23aa)::eGFP.

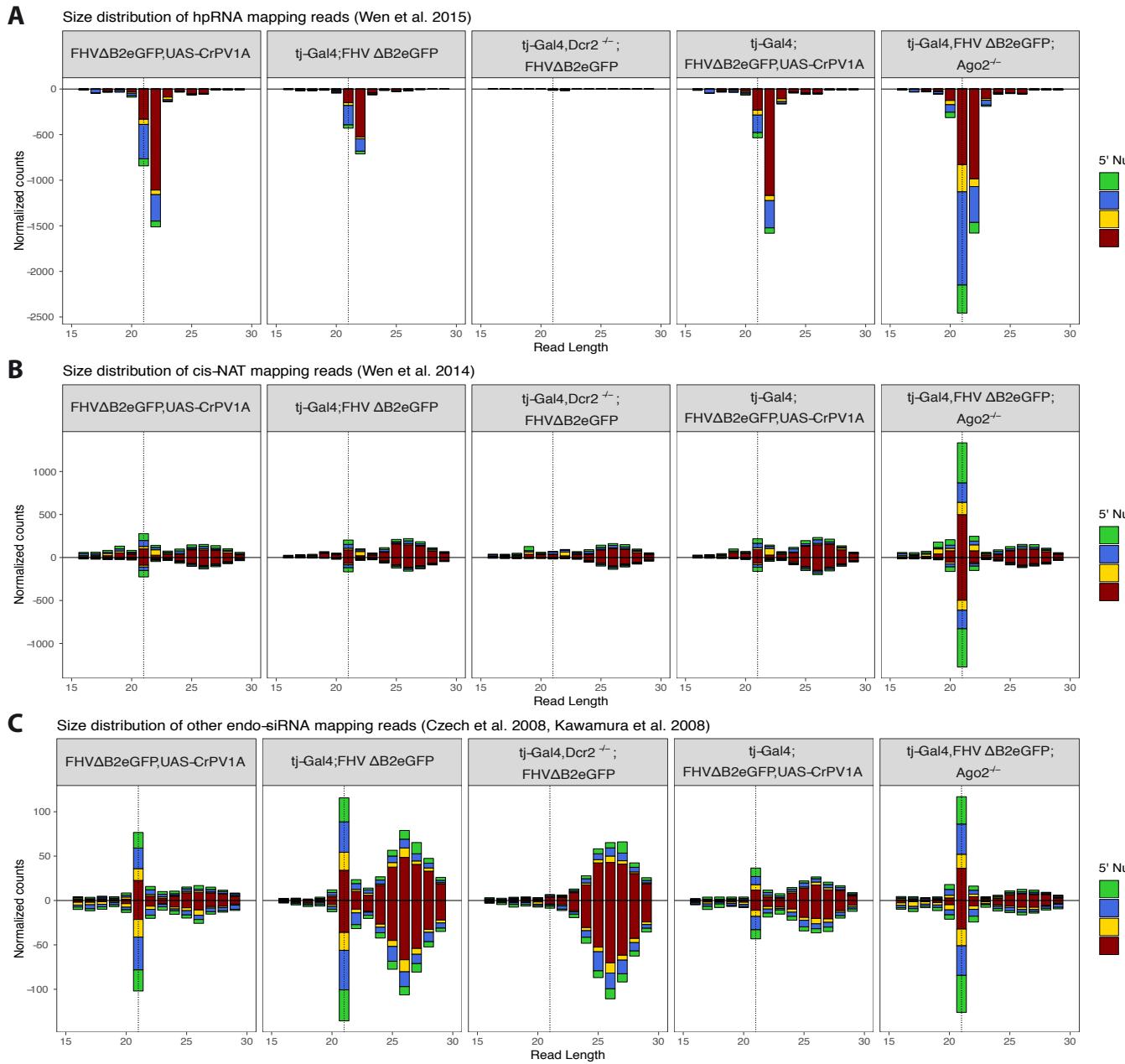


Figure S3 - small RNA profiles of endo-siRNA generating loci. Size distribution and 5' nucleotide of small RNA reads mapping to **(A)** hairpin RNA (Wen et al. 2015, Kawamura et al. 2008) **(B)** cis-NATs (defined in Han et al. 2015 and Wen et al. 2014) or **(C)** other endo-siRNA generating loci (Czech et al. 2008, Kawamura et al. 2008) in small RNA libraries prepared from ovaries of *Drosophila melanogaster*. Reads are normalized to total reads, excluding microRNAs and ribosomal RNAs. Note the depletion of 21 nucleotide reads (indicated by the dotted line) for all classes of endo-siRNAs in the libraries from dcr2 null mutants (tj-Gal4,Dcr2 $^{-/-}$,FHV Δ B2eGFP panels) and their accumulation in the Ago2 null mutants (tj-Gal4, FHV Δ B2eGFP;Ago2 $^{-/-}$ panels).

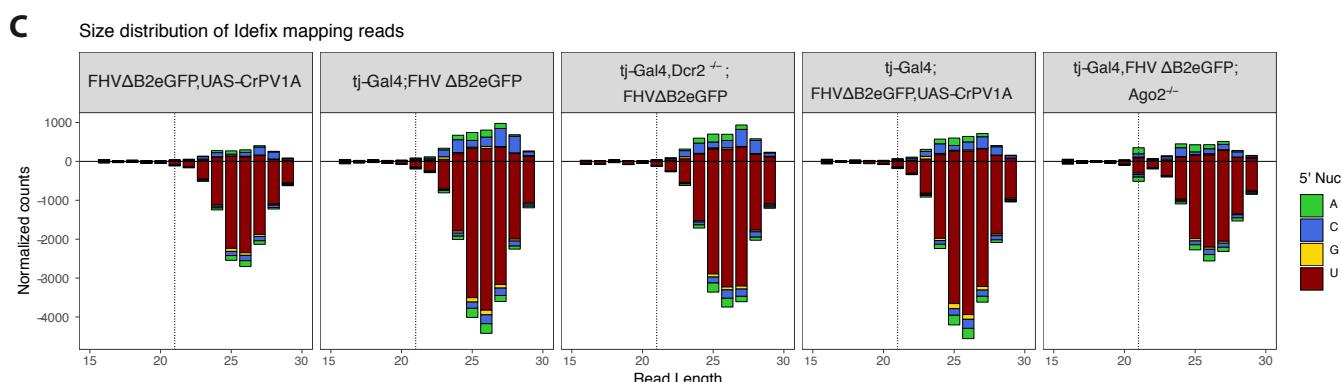
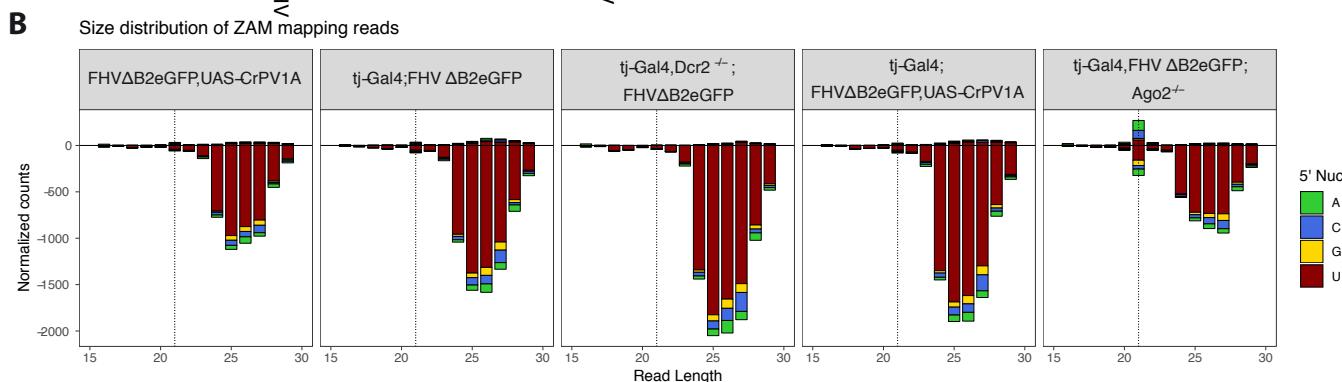
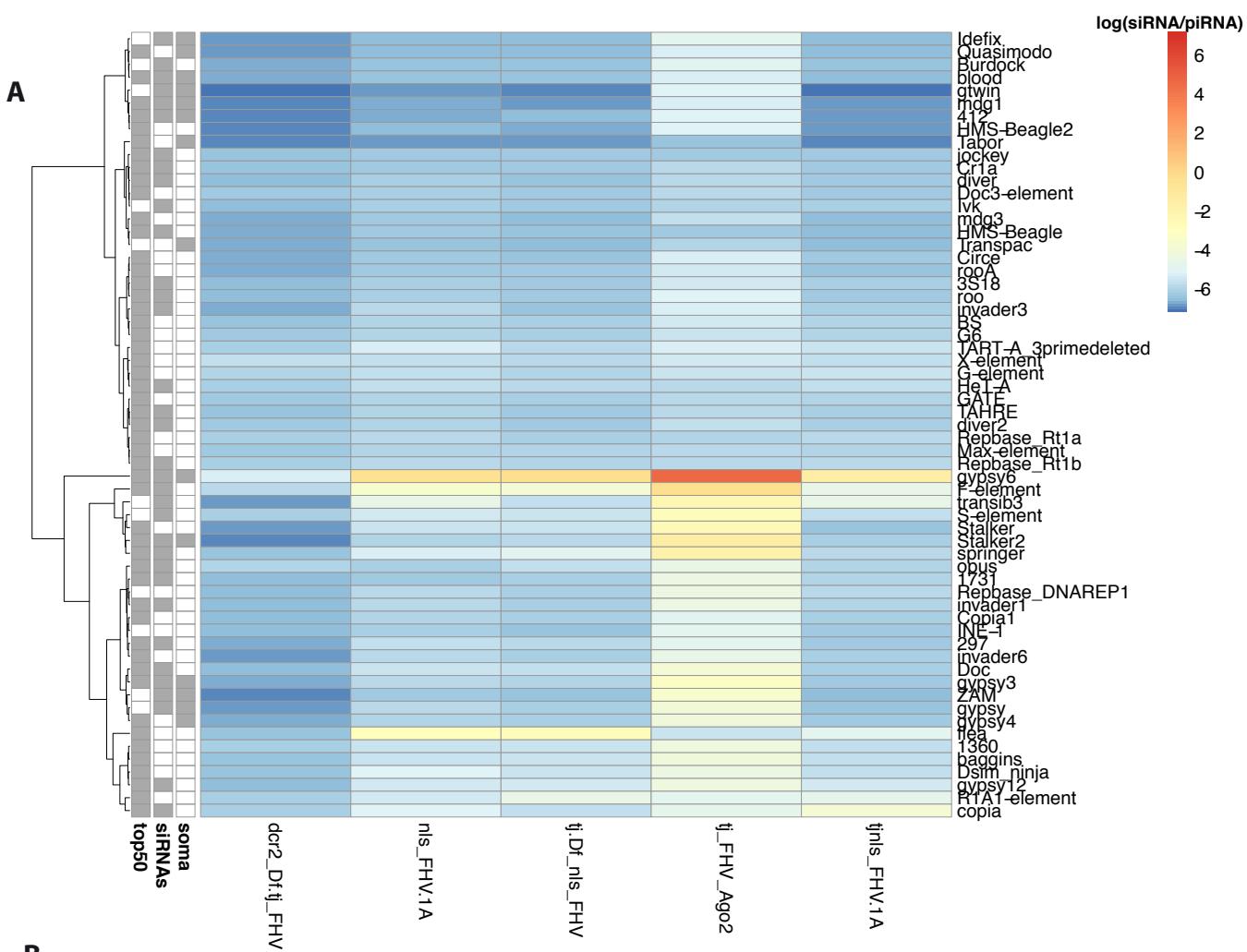


Figure S4 - Transposable element transcripts are processed by the siRNA pathway. (A) Heatmap of log(ratios) between siRNA- and piRNA-like reads mapping to transposable elements(TE). Depicted are the 50 most expressed TEs in the small RNA libraries prepared from ovaries of *Drosophila melanogaster* of the indicated genotypes. In addition, TEs whose transcripts are known to be processed by the endo-siRNA pathway (Ghildiyal et al. 2008, Czech et al. 2008, Kawamura et al. 2008, Chung et al. 2008) or expressed in somatic tissues of the ovaries (Malone et al. 2009). In addition are represented. Below are depicted the size distribution and 5' nucleotide of small RNA reads mapping to the TE's (B) ZAM and (C) Idefix, two TE's known to be expressed in the follicular somatic cells of *D. melanogaster* ovaries.

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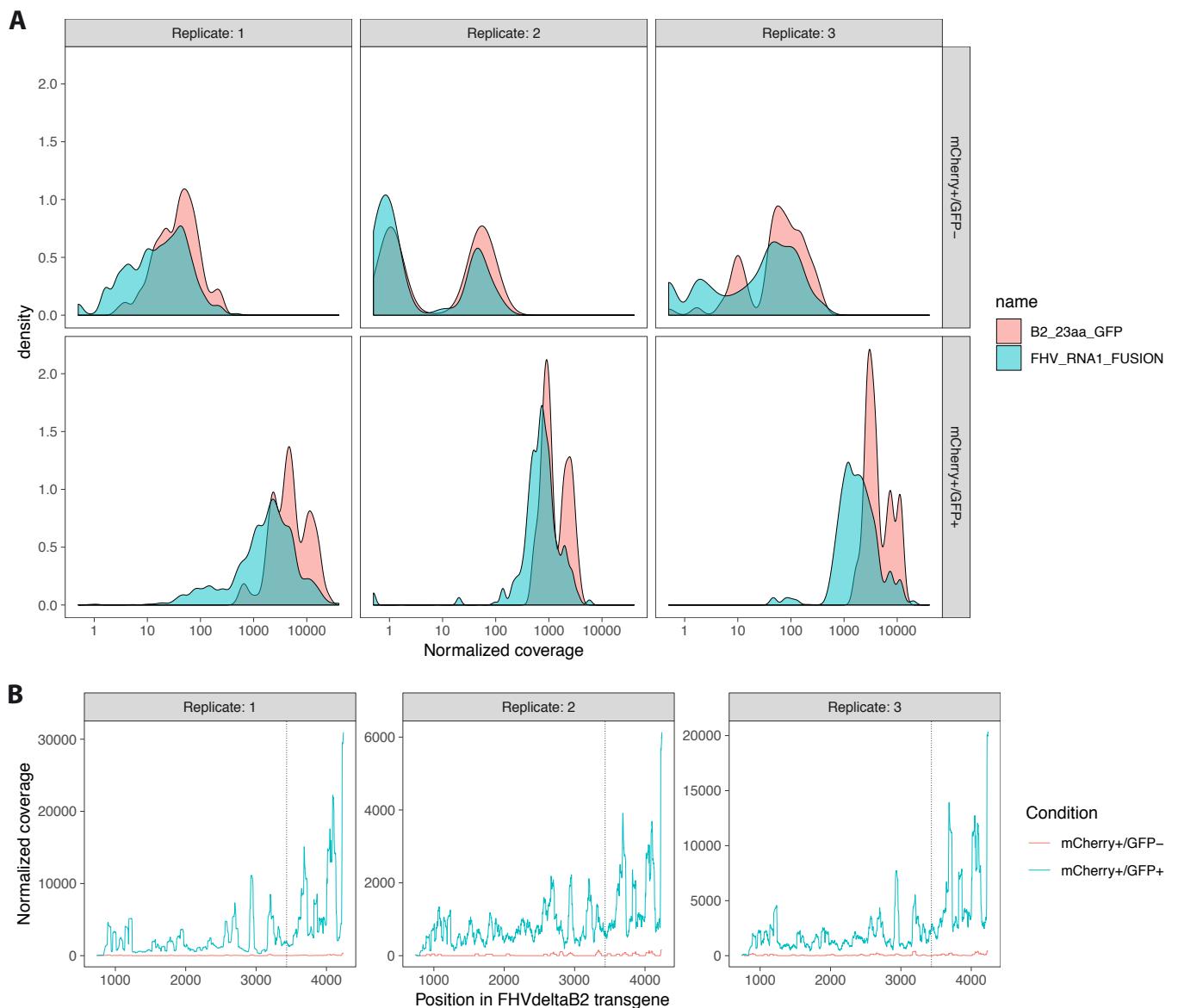


Figure S5 - Coverage profiles of FHV Δ B2eGFP in replicon restrictive and permissive cell fractions. Shown are the (A) density plots and (B) across genome coverage FHV Δ B2eGFP transcripts - RNA1 (FHV_RNA1_FUSION) and RNA3 (B2_23aa_eGFP). The dotted line in panel B represents the transcription start site of RNA3. The different subpanels represent independent replicates of RNAseq libraries from FHV Δ B2eGFP restrictive (mCherry+/GFP-) and permissive (mCherry+/GFP+) follicular somatic cells of tj-Gal4,UAS-mCherry::NLS; UAS-FHV Δ B2eGFP,UAS-CrPV-1A flies. Values are normalized to million mapped positions.

Martins_Tables_Supplementary.xlsx

Table S1 - Statistics of the small RNA sequencing analysis.

Table S2 - Reads mapping to hairpin RNA loci in small RNA libraries.

Table S3 - Differentially expressed genes between FHV Δ B2eGFP restrictive (mCherry+GFP-) and permissive (mCherry+GFP+) follicular somatic cells of *tj*-Gal4,UAS-mCherry::NLS; UAS-FHV Δ B2eGFP,UAS-CrPV-1A flies.

Table S4 - Gene expression (read counts) in the double negative cell fraction (mCherry-GFP-), FHV Δ B2eGFP restrictive (mCherry+GFP-) and permissive (mCherry+GFP+) follicular somatic cells of *tj*-Gal4,UAS-mCherry::NLS; UAS-FHV Δ B2eGFP,UAS-CrPV-1A flies.

Table S5 - Normalized gene expression (backtransformed rlog(counts)) in the double negative cell fraction (mCherry-GFP-), FHV Δ B2eGFP restrictive (mCherry+GFP-) and permissive (mCherry+GFP+) follicular somatic cells of *tj*-Gal4,UAS-mCherry::NLS; UAS-FHV Δ B2eGFP,UAS-CrPV-1A flies.